

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/934,254DATE: 03/26/98
TIME: 18:19:17

INPUT SET: S24406.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Thomas, Terry L.

(ii) TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
DELTA 6-DESATURASE

(iii) NUMBER OF SEQUENCES: 27

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Scully, Scott, Murphy & Presser

(B) STREET: 400 Garden City Plaza

(C) CITY: Garden City

(D) STATE: New York

(E) COUNTRY: United States

(F) ZIP: 11530

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Presser, Leopold

(B) REGISTRATION NUMBER: 19,827

(C) REFERENCE/DOCKET NUMBER: 8383ZYXWVU

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (516) 742-4343

(B) TELEFAX: (516) 742-4366

(C) TELEX: 230 901 SANS UR

(2) INFORMATION FOR SEQ ID NO:1:

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PATENT APPLICATION US/08/934,254DATE: 03/26/98
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47

48

(i) SEQUENCE CHARACTERISTICS:

49

50

(A) LENGTH: 3588 base pairs

51

(B) TYPE: nucleic acid

52

(C) STRANDEDNESS: both

53

(D) TOPOLOGY: linear

54

55

(ii) MOLECULE TYPE: DNA (genomic)

56

57

(ix) FEATURE:

58

59

(A) NAME/KEY: CDS

60

(B) LOCATION: 2002..3081

61

62

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

63

64

GCTAGCCACC AGTGACGATG CCTTGAATTT GGCCATTCTG ACCCAGGCCC GTATTCTGAA 60

65

66

TCCCCGCATT CGCATTGTTA ATCGTTTGTT CAACCATGCC CTGGGTAAAC GTTTAGACAC 120

67

68

CACCTTGCCA GACCACGTTA GTTTGAGTGT TTCCGCCCTG GCGGCCCCGA TTTTTCCTT 180

69

70

TGCGGCTTTG GGCAATCAGG CGATCGGGCA ATTGCGTTTG TTTGACCAGA CTTGGCCCAT 240

71

72

TCAGGAAATT GTCATTCACC AAGACCATCC CTGGCTCAAT TTACCCCTGG CGGATTTATG 300

73

74

GGATGATCCG AGCCGAATGT TGATCTATTA CCTACCGGCC CACAGTGAAA CGGATTTAGT 360

75

76

AGGCGCAGTG GTGAATAATT TAACGTTGCA ATCTGGGGAC CATTTAATAG TGGGACAAAA 420

77

78

ACCCCAACCC AAGACCAAAC GGCGATCGCC TTGGCGCAA TTTTCCAAAC TGATTACCAA 480

79

80

CCTGCGGGAG TATCAGCGGT ATGTCCAACA GGTGATATGG GTGGTGTTGT TTTTATTGTT 540

81

82

GATGATTTTT CTGGCCACCT TCATCTACGT TTCCATTGAT CAACATATTG CCCCAGTGGA 600

83

84

CGCGTTGTAT TTTTCCGTGG GCATGATTAC CGGGGCCGGT GGCAAGGAAG AGGTGGCCGA 660

85

86

AAAGTCCCC GATATCATCA AAGTATTCAC AGTGGTGATG ATGATCGCCG GGGCGGGGGT 720

87

88

GATTGGTATT TGTTATGCCC TACTGAATGA TTTCATCCTT GGCAGTCGCT TTAGTCAGTT 780

89

90

TTTGGATGCG GCCAAGTTAC CCGATCGCCA TCACATCATC ATTTGTGGGC TGGGGGGAGT 840

91

92

GAGCATGGCC ATTATTGAAG AGTTAATTCA CCAGGGCCAT GAAATTGTGG TAATCGAAAA 900

93

94

GGATACAGAT AATCGTTTCT TGCATACGGC CCGCTCCCTG GGGGTGCCCC TAATTGTGGA 960

95

96

GGATGCCCCG CTAGAAAGAA CGTTGGCCTG CGCCAATATC AACCGAGCCG AAGCCATTGT 1020

97

98

GGTGGCCACC AGCGACGACA CCGTTAACTT GGAAATTGGC CTAAGTGCCA AGGCGATCGC 1080

99

RAW SEQUENCE LISTING PATENT APPLICATION US/08/934,254

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| | | |
|-----|--|------|
| 100 | CCCTAGCCTG CCAGTGGTGT TGC GTTGCCA GGATGCCCAG TTTAGCCTGT CCCTGCAGGA | 1140 |
| 101 | | |
| 102 | AGTATTTGAA TTTGAAACGG TGCTTTGTCC GGC GGAATTG GCCACCTATT CCTTTGCGGC | 1200 |
| 103 | | |
| 104 | GGCGGCCCTG GGGGGCAAAA TTTTGGGCAA CGGCATGACC GATGATTTGC TGTGGGTAGC | 1260 |
| 105 | | |
| 106 | CCTAGCCACC TTAATCACTC CTAACCATCC CTTTGCCGAC CAATTGGTTA AAATTGCAGC | 1320 |
| 107 | | |
| 108 | CCAAAAGTCT GATTTTCGTTC CCCTCTATCT AGAACGGGGT GGCAAAACCA TCCATAGCTG | 1380 |
| 109 | | |
| 110 | GGAATTATTG GGTACCCATC TCGACTCTGG AGACGTGTTG TATTTAACCA TGCCCGCCAC | 1440 |
| 111 | | |
| 112 | TGCCCTAGAG CAACTTTGGC GATCGCCCCG TGCCACTGCT GATCCTCTGG ACTCTTTTTT | 1500 |
| 113 | | |
| 114 | GGTTTAGCAT GGGGGGATGG AACTCTTGAC TCGGCCCAAT GGTGATCAAG AAAGAACGCT | 1560 |
| 115 | | |
| 116 | TTGTCTATGT TTAGTATTTT TAAGTTAACC AACAGCAGAG GATAACTTCC AAAAGAAATT | 1620 |
| 117 | | |
| 118 | AAGCTCAAAA AGTAGCAAAA TAAGTTTAAT TCATAACTGA GTTTTACTGC TAAACAGCGG | 1680 |
| 119 | | |
| 120 | TGCAAAAAAG TCAGATAAAA TAAAAGCTTC ACTTCGGTTT TATATTGTGA CCATGGTTCC | 1740 |
| 121 | | |
| 122 | CAGGCATCTG CTCTAGGGAG TTTTCCGCT GCCTTTAGAG AGTATTTTCT CCAAGTCGGC | 1800 |
| 123 | | |
| 124 | TAACTCCCC ATTTTTAGGC AAAATCATAT ACAGACTATC CCAATATTGC CAGAGCTTTG | 1860 |
| 125 | | |
| 126 | ATGACTCACT GTAGAAGGCA GACTAAAATT CTAGCAATGG ACTCCCAGTT GGAATAAATT | 1920 |
| 127 | | |
| 128 | TTTAGTCTCC CCCGGCGCTG GAGTTTTTTT GTAGTTAATG GCGGTATAAT GTGAAAGTTT | 1980 |
| 129 | | |
| 130 | TTTATCTATT TAAATTTATA A ATG CTA ACA GCG GAA AGA ATT AAA TTT ACC | 2031 |
| 131 | | |
| 132 | | |
| 133 | | |
| 134 | CAG AAA CGG GGG TTT CGT CGG GTA CTA AAC CAA CGG GTG GAT GCC TAC | 2079 |
| 135 | Gln Lys Arg Gly Phe Arg Arg Val Leu Asn Gln Arg Val Asp Ala Tyr | |
| 136 | | |
| 137 | | |
| 138 | TTT GCC GAG CAT GGC CTG ACC CAA AGG GAT AAT CCC TCC ATG TAT CTG | 2127 |
| 139 | Phe Ala Glu His Gly Leu Thr Gln Arg Asp Asn Pro Ser Met Tyr Leu | |
| 140 | | |
| 141 | | |
| 142 | AAA ACC CTG ATT ATT GTG CTC TGG TTG TTT TCC GCT TGG GCC TTT GTG | 2175 |
| 143 | Lys Thr Leu Ile Ile Val Leu Trp Leu Phe Ser Ala Trp Ala Phe Val | |
| 144 | | |
| 145 | | |
| 146 | CTT TTT GCT CCA GTT ATT TTT CCG GTG CGC CTA CTG GGT TGT ATG GTT | 2223 |
| 147 | Leu Phe Ala Pro Val Ile Phe Pro Val Arg Leu Leu Gly Cys Met Val | |
| 148 | | |
| 149 | | |
| 150 | TTG GCG ATC GCC TTG GCG GCC TTT TCC TTC AAT GTC GGC CAC GAT GCC | 2271 |
| 151 | Leu Ala Ile Ala Leu Ala Ala Phe Ser Phe Asn Val Gly His Asp Ala | |
| 152 | | |

INPUT SET: S24406.raw

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|------|
| 153 | | | | | | | | | | | | | | | | | | |
| 154 | AAC | CAC | AAT | GCC | TAT | TCC | TCC | AAT | CCC | CAC | ATC | AAC | CGG | GTT | CTG | GGC | | 2319 |
| 155 | Asn | His | Asn | Ala | Tyr | Ser | Ser | Asn | Pro | His | Ile | Asn | Arg | Val | Leu | Gly | | |
| 156 | | | | | 95 | | | | | 100 | | | | | 105 | | | |
| 157 | | | | | | | | | | | | | | | | | | |
| 158 | ATG | ACC | TAC | GAT | TTT | GTC | GGG | TTA | TCT | AGT | TTT | CTT | TGG | CGC | TAT | CGC | | 2367 |
| 159 | Met | Thr | Tyr | Asp | Phe | Val | Gly | Leu | Ser | Phe | Leu | Trp | Arg | Tyr | Arg | | | |
| 160 | | | | 110 | | | | | 115 | | | | 120 | | | | | |
| 161 | | | | | | | | | | | | | | | | | | |
| 162 | CAC | AAC | TAT | TTG | CAC | CAC | ACC | TAC | ACC | AAT | ATT | CTT | GGC | CAT | GAC | GTG | | 2415 |
| 163 | His | Asn | Tyr | Leu | His | His | Thr | Tyr | Thr | Asn | Ile | Leu | Gly | His | Asp | Val | | |
| 164 | | | 125 | | | | | 130 | | | | | 135 | | | | | |
| 165 | | | | | | | | | | | | | | | | | | |
| 166 | GAA | ATC | CAT | GGA | GAT | GGC | GCA | GTA | CGT | ATG | AGT | CCT | GAA | CAA | GAA | CAT | | 2463 |
| 167 | Glu | Ile | His | Gly | Asp | Gly | Ala | Val | Arg | Met | Ser | Pro | Glu | Gln | Glu | His | | |
| 168 | | 140 | | | | | 145 | | | | | 150 | | | | | | |
| 169 | | | | | | | | | | | | | | | | | | |
| 170 | GTT | GGT | ATT | TAT | CGT | TTC | CAG | CAA | TTT | TAT | ATT | TGG | GGT | TTA | TAT | CTT | | 2511 |
| 171 | Val | Gly | Ile | Tyr | Arg | Phe | Gln | Gln | Phe | Tyr | Ile | Trp | Gly | Leu | Tyr | Leu | | |
| 172 | | 155 | | | | 160 | | | | | 165 | | | | | 170 | | |
| 173 | | | | | | | | | | | | | | | | | | |
| 174 | TTC | ATT | CCC | TTT | TAT | TGG | TTT | CTC | TAC | GAT | GTC | TAC | CTA | GTG | CTT | AAT | | 2559 |
| 175 | Phe | Ile | Pro | Phe | Tyr | Trp | Phe | Leu | Tyr | Asp | Val | Tyr | Leu | Val | Leu | Asn | | |
| 176 | | | | | 175 | | | | | 180 | | | | | 185 | | | |
| 177 | | | | | | | | | | | | | | | | | | |
| 178 | AAA | GGC | AAA | TAT | CAC | GAC | CAT | AAA | ATT | CCT | CCT | TTC | CAG | CCC | CTA | GAA | | 2607 |
| 179 | Lys | Gly | Lys | Tyr | His | Asp | His | Lys | Ile | Pro | Pro | Phe | Gln | Pro | Leu | Glu | | |
| 180 | | | | 190 | | | | | 195 | | | | | 200 | | | | |
| 181 | | | | | | | | | | | | | | | | | | |
| 182 | TTA | GCT | AGT | TTG | CTA | GGG | ATT | AAG | CTA | TTA | TGG | CTC | GGC | TAC | GTT | TTC | | 2655 |
| 183 | Leu | Ala | Ser | Leu | Leu | Gly | Ile | Lys | Leu | Leu | Trp | Leu | Gly | Tyr | Val | Phe | | |
| 184 | | | 205 | | | | | 210 | | | | | 215 | | | | | |
| 185 | | | | | | | | | | | | | | | | | | |
| 186 | GGC | TTA | CCT | CTG | GCT | CTG | GGC | TTT | TCC | ATT | CCT | GAA | GTA | TTA | ATT | GGT | | 2703 |
| 187 | Gly | Leu | Pro | Leu | Ala | Leu | Gly | Phe | Ser | Ile | Pro | Glu | Val | Leu | Ile | Gly | | |
| 188 | | 220 | | | | | 225 | | | | | 230 | | | | | | |
| 189 | | | | | | | | | | | | | | | | | | |
| 190 | GCT | TCG | GTA | ACC | TAT | ATG | ACC | TAT | GGC | ATC | GTG | GTT | TGC | ACC | ATC | TTT | | 2751 |
| 191 | Ala | Ser | Val | Thr | | | | | | | | | | | | | | |

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206  GGT TTA AAT CAC CAA GTT ACC CAC CAT CTT TTC CCC AAT ATT TGT CAT      2943
207  Gly Leu Asn His Gln Val Thr His His Leu Phe Pro Asn Ile Cys His
208      300                      305                      310
209
210  ATT CAC TAT CCC CAA TTG GAA AAT ATT ATT AAG GAT GTT TGC CAA GAG      2991
211  Ile His Tyr Pro Gln Leu Glu Asn Ile Ile Lys Asp Val Cys Gln Glu
212  315                      320                      325                      330
213
214  TTT GGT GTG GAA TAT AAA GTT TAT CCC ACC TTC AAA GCG GCG ATC GCC      3039
215  Phe Gly Val Glu Tyr Lys Val Tyr Pro Thr Phe Lys Ala Ala Ile Ala
216      335                      340                      345
217
218  TCT AAC TAT CGC TGG CTA GAG GCC ATG GGC AAA GCA TCG TGACATTGCC      3088
219  Ser Asn Tyr Arg Trp Leu Glu Ala Met Gly Lys Ala Ser
220      350                      355
221
222  TTGGGATTGA AGCAAAATGG CAAAATCCCT CGTAAATCTA TGATCGAAGC CTTTCTGTGTG      3148
223
224  CCCGCCGACC AAATCCCCGA TGCTGACCAA AGGTTGATGT TGGCATTGCT CCAAACCCAC      3208
225
226  TTTGAGGGGG TTCATTGGCC GCAGTTTCAA GCTGACCTAG GAGGCAAAGA TTGGGTGATT      3268
227
228  TTGCTCAAAT CCGCTGGGAT ATTGAAAGGC TTCACCACCT TTGGTTTCTA CCCTGCTCAA      3328
229
230  TGGGAAGGAC AAACCGTCAG AATTGTTTAT TCTGGTGACA CCATCACCGA CCCATCCATG      3388
231
232  TGGTCTAACC CAGCCCTGGC CAAGGCTTGG ACCAAGGCCA TGCAAATTCT CCACGAGGCT      3448
233
234  AGGCCAGAAA AATTATATTG GCTCCTGATT TCTTCCGGCT ATCGCACCTA CCGATTTTTG      3508
235
236  AGCATTTTTG CCAAGGAATT CTATCCCCAC TATCTCCATC CCACTCCCCC GCCTGTACAA      3568
237
238  AATTTTATCC ATCAGCTAGC      3588
239
240
241  (2) INFORMATION FOR SEQ ID NO:2:
242
243      (i) SEQUENCE CHARACTERISTICS:
244
245          (A) LENGTH: 359 amino acids
246          (B) TYPE: amino acid
247          (D) TOPOLOGY: linear
248
249      (ii) MOLECULE TYPE: protein
250
251      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
252
253  Met Leu Thr Ala Glu Arg Ile Lys Phe Thr Gln Lys Arg Gly Phe Arg
254      1                      5                      10                      15
255
256  Arg Val Leu Asn Gln Arg Val Asp Ala Tyr Phe Ala Glu His Gly Leu
257      20                      25                      30
258

```

INPUT SET: S24406.raw

***** PREVIOUSLY ERRORED SEQUENCES - EDITED *****

878 (2) INFORMATION FOR SEQ ID NO:25:

879

880 (i) SEQUENCE CHARACTERISTICS:

881

882 (A) LENGTH: 5 amino acids

883 (B) TYPE: amino acid

884 (D) TOPOLOGY: linear

885

886 (ii) MOLECULE TYPE: Peptide

887

888 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

889

890 His Val Pro His His

891

1

5

892

893

1045 (2) INFORMATION FOR SEQ ID NO:27:

1046

1047 (i) SEQUENCE CHARACTERISTICS:

1048 (A) LENGTH: 452 amino acids

1049 (B) TYPE: amino acid

1050 (D) TOPOLOGY: linear

1051

1052 (ii) MOLECULE TYPE: protein

1053

1054 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

1055

1056 Met Glu Gly Glu Ala Lys Lys Tyr Ile Thr Ala Glu Asp Leu Arg Arg

1057

1

5

10

15

1058

1059 His Asn Lys Ser Gly Asp Leu Trp Ile Ser Ile Gln Gly Lys Val Tyr

1060

20

25

30

1061

1062 Asp Cys Ser Arg Trp Ala Ala Glu His Pro Gly Gly Glu Val Pro Leu

1063

35

40

45

1064

1065 Leu Ser Leu Ala Gly Gln Asp Val Thr Asp Ala Phe Ile Ala Tyr His

1066

50

55

60

1067

1068 Pro Gly Thr Ala Trp Arg His Leu Asp Pro Leu Phe Thr Gly Tyr Tyr

1069

65

70

75

80

1070

1071 Tyr Leu Lys Asp Phe Glu Val Ser Glu Ile Ser Lys Asp Tyr Arg Arg

1072

85

90

95

1073

1074 Leu Leu Asn Glu Met Ser Arg Ser Gly Ile Phe Glu Lys Lys Gly His

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| | 100 | 105 | 110 |
|------|---|-----|-----|
| 1075 | | | |
| 1076 | | | |
| 1077 | His Ile Met Trp Thr Phe Val Gly Val Ala Val Met Met Ala Ala Ile | | |
| 1078 | 115 | 120 | 125 |
| 1079 | | | |
| 1080 | Val Tyr Gly Val Leu Ala Ser Glu Ser Val Gly Val His Met Leu Cys | | |
| 1081 | 130 | 135 | 140 |
| 1082 | | | |
| 1083 | Gly Ala Leu Leu Gly Leu Leu Trp Ile Gln Ala Ala Tyr Val Gly His | | |
| 1084 | 145 | 150 | 155 |
| 1085 | | | |
| 1086 | Asp Ser Gly His Tyr Gln Val Met Pro Thr Arg Gly Tyr Asn Arg Ile | | |
| 1087 | 165 | 170 | 175 |
| 1088 | | | |
| 1089 | Thr Gln Leu Ile Ala Gly Asn Ile Leu Thr Gly Ile Ser Ile Ala Trp | | |
| 1090 | 180 | 185 | 190 |
| 1091 | | | |
| 1092 | Trp Lys Trp Thr His Asn Ala His His Leu Ala Cys Asn Ser Leu Asp | | |
| 1093 | 195 | 200 | 205 |
| 1094 | | | |
| 1095 | Tyr Asp Pro Asp Leu Gln His Ile Pro Val Phe Ala Val Ser Thr Arg | | |
| 1096 | 210 | 215 | 220 |
| 1097 | | | |
| 1098 | Leu Phe Asn Ser Ile Thr Ser Val Phe Tyr Gly Arg Val Leu Lys Phe | | |
| 1099 | 225 | 230 | 235 |
| 1100 | | | |
| 1101 | Asp Glu Val Ala Arg Phe Leu Val Ser Tyr Gln His Trp Thr Tyr Tyr | | |
| 1102 | 245 | 250 | 255 |
| 1103 | | | |
| 1104 | Pro Val Met Ile Phe Gly Arg Val Asn Leu Phe Ile Gln Thr Phe Leu | | |
| 1105 | 260 | 265 | 270 |
| 1106 | | | |
| 1107 | Leu Leu Leu Thr Arg Arg Asp Val Pro Asp Arg Ala Leu Asn Leu Met | | |
| 1108 | 275 | 280 | 285 |
| 1109 | | | |
| 1110 | Gly Ile Ala Val Phe Trp Thr Trp Phe Pro Leu Phe Val Ser Cys Leu | | |
| 1111 | 290 | 295 | 300 |
| 1112 | | | |
| 1113 | Pro Asn Trp Pro Glu Arg Phe Gly Phe Val Leu Ile Ser Phe Ala Val | | |
| 1114 | 305 | 310 | 315 |
| 1115 | | | |
| 1116 | Thr Ala Ile Gln His Val Gln Phe Thr Leu Asn His Phe Ser Gly Asp | | |
| 1117 | 325 | 330 | 335 |
| 1118 | | | |
| 1119 | Thr Tyr Val Gly Pro Pro Lys Gly Asp Asn Trp Phe Glu Lys Gln Thr | | |
| 1120 | 340 | 345 | 350 |
| 1121 | | | |
| 1122 | Lys Gly Thr Ile Asp Ile Thr Cys Pro Pro Trp Met Asp Trp Phe Phe | | |
| 1123 | 355 | 360 | 365 |
| 1124 | | | |
| 1125 | Gly Gly Leu Gln Phe Gln Leu Glu His His Leu Phe Pro Arg Leu Pro | | |
| 1126 | 370 | 375 | 380 |
| 1127 | | | |

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| | | |
|------|---|-------------|
| 1128 | Arg Gly Gln Leu Arg Lys Ile Ala Pro Leu Ala Arg Asp Leu Cys Lys | |
| 1129 | 385 | 390 395 400 |
| 1130 | | |
| 1131 | Lys His Gly Met Pro Tyr Arg Ser Phe Gly Phe Trp Asp Asp Ala Asn | |
| 1132 | | 405 410 415 |
| 1133 | | |
| 1134 | Val Arg Thr Ile Arg Thr Leu Arg Asp Ala Ala Val Gln Ala Arg Asp | |
| 1135 | | 420 425 430 |
| 1136 | | |
| 1137 | Leu Asn Ser Ala Pro Cys Pro Lys Lys Leu Gly Tyr Gly Glu Ala Tyr | |
| 1138 | | 435 440 445 |
| 1139 | | |
| 1140 | Asn Thr His Gly | |
| 1141 | | 450 |
| 1142 | | |

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Line

Error

Original Text